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1146



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HTXOO15	7011	869261	AP000944	36204	1-773
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1162



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HBJAB15	9522	660552	AP001931	42442	1-1266
HBJAB15	9522	660552	AP000727	42443	1-1264
HBJAB15	9522	660552	AP001931	42444	1-366
HBJAB15	9522	660552	AP001931	42445	1-308
HBJAB15	9522	660552	AP000727	42446	1-366
HBJAB15	9522	660552	AP000727	42447	1-308
HBD4E47	9523	720008	AL353776	42448	1-1591
HBD4E47	9523	720008	AL353776	42449	1-490
HBDAD16	9525	661560	AC013396	42450	1-1371
HBDAD16	9525	661560	AC013396	42451	1-296
HBDAD16	9525	661560	AC013396	42452	1-204
HBCCO10	9526	963157	AC009634	42453	1-575
HBCCO10	9526	963157	AC011721	42454	1-575
HBCCO10	9526	963157	AC009634	42455	1-206
HBCCO10	9526	963157	AC011721	42456	1-206
HBCCO10	9526	963157	AC011721	42457	1-86
HBCCJ05	9527	930956	AC068322	42458	1-600
HBCCJ05	9527	930956	AC027243	42459	1-600
HBCCJ05	9527	930956	AC024059	42460	1-600
HBCCJ05	9527	930956	AC010868	42461	1-584
HBCCJ05	9527	930956	AC068322	42462	1-424
HBCCJ05	9527	930956	AC027243	42463	1-456
HBCCJ05	9527	930956	AC068322	42464	1-460
					1112-1585
HBCCJ05	9527	930956	AC027243	42465	1-460
					1112-1585
HBCCJ05	9527	930956	AC024059	42466	1-456
HBCCJ05	9527	930956	AC010868	42467	1-385
HBCCJ05	9527	930956	AC010868	42468	1-335
HBCCD06	9529	938319	AC007783	42469	1-2334
					2508-3084
					3578-3890



					4198-4294 4376-4623 4712-5349 5369-6088 6527-7107 7298-7392 7730-7846 9147-9476 10487-10575 10791-11298 11485-11601 11783-13009 13207-13501 13540-13772 14439-14800 14923-14983 15133-15355 15485-15653 16750-16805 16894-17078 17162-17219 18003-18089 21085-21146 21358-21501
HBCCD06	9529	938319	AC007783	42470	1-308
HBCCD06	9529	938319	AC007783	42471	1-1024
HBCCB51	9530	975256	AL139353	42472	1-71 265-794 1791-2077 2409-2656
HBCBN51	9532	952057	AC073846	42473	1-141 323-951 1073-1625 1640-2371
HBCBN51	9532	952057	AC073846	42474	1-285
HBCBF12	9535	969578	AC068735	42475	1-530
HBCBF12	9535	969578	AC021725	42476	1-534
HBCBF12	9535	969578	AL021368	42477	1-382 762-1102 1231-1761
HBCBF12	9535	969578	AC068735	42478	1-342
HBCBF12	9535	969578	AC021725	42479	1-342
HBCBF12	9535	969578	AC068735	42480	1-659
HBCBF12	9535	969578	AC021725	42481	1-679
HBCBF12	9535	969578	AL021368	42482	1-664
HBCBF12	9535	969578	AL021368	42483	1-307
HBCBE57	9536	848322	AL031666	42484	1-1235
HBCBE57	9536	848322	AL031666	42485	1-508
HBCBE57	9536	848322	AL031666	42486	1-648
HBCBB22	9537	848325	AC010735	42487	1-900
HBCAT10	9539	968195	AL357521	42488	1-374
HBCAT10	9539	968195	AL021528	42489	1-374
HBCAT10	9539	968195	AL357521	42490	1-689
HBCAT10	9539	968195	AL357521	42491	1-355
HBCAT10	9539	968195	AL021528	42492	1-689
HBCAT10	9539	968195	AL021528	42493	1-355

HBCAS32	9540	699489	AC007101	42494	1-215 867-1214 1226-2260 2359-2415
HBCAQ85	9541	783431	AC019071	42495	1-831 1116-1365 1600-1920 2161-2334 2902-3156 3364-3836 4074-4278 4306-4417 4485-4581 4693-4853 4995-5264 5758-5863 6411-6509 6551-6922
HBCAQ85	9541	783431	AC019071	42496	1-412
HASCG58	9543	738423	AC011116	42497	1-869
HASCG58	9543	738423	AC078794	42498	1-870
HASCG58	9543	738423	AC011116	42499	1-971
HASCG58	9543	738423	AC078794	42500	1-623
HASCG58	9543	738423	AC011116	42501	1-623
HASAW90	9544	789112	AC010234	42502	1-2931
HASAW90	9544	789112	AC021464	42503	1-58 332-547 909-1209 2280-2634 3445-3539 4477-4620 7577-10496 12087-13447 13462-15091 15142-16137
HASAW90	9544	789112	AC021464	42504	1-506
HASAC10	9546	968746	AC007677	42505	1-477
HASAC10	9546	968746	AC007677	42506	1-1410

[052] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

## **TABLE 2**

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HAMHB21	961376	11	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	100	497	916
HBDAC79	935414	26	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	102.6	94	342
			blastx.14	(AL021958) fadE9 [Mycobacterium tuberculosis]	gi 2911026 emb CAA 17519.1	62% 51% 64% 35%	94 250 348 6	255 384 422 89
HBJAG72	722723	32	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.32	83	115
HBJGT92	919507	107	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	7.68	377	436
HBJJY20	669519	141	HMMER 2.1.1	PFAM: Orn/Lys/Arg decarboxylase	PF01276	53.1	49	162
HBMUBU24	677240	234	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.72	139	192
HBMZ71	880580	238	HMMER 1.8	PFAM: von Willebrand factor type D domain	PF00094	26.52	200	526
HBMDC16	888206	258	blastx.2	Butyrophilin-like protein BUTR-1.	sp AAF72554 AAF72 554	50%	19	315
HBMUO90	928078	294	blastx.14	Zfp61p [Mus musculus]	gi 887887 gb AAC52 290.1	84% 53%	24 154	119 243
HBMXE31	573323	317	HMMER 1.8	PFAM: Gonadotropin- releasing hormones	PF00446	10.78	112	141
HCFCF47	894415	372	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	89.54	20	295
HCFCJ21	671028	374	HMMER	PFAM: Core histones	PF00125	12.79	123	188

			1.8	H2A, H2B, H3 and H4 p34 protein [Rattus sp.]	gi 534876 dbj BAA02786.1				
HCFL95	945122	391	blastx.14	(AF079098) arginine-tRNA-protein transferase 1-1p; ATE1-lp [Homo sapiens]	gi 3806094 gb AAD12366.1	87%	5	126	191
HCUAL07	953876	449	blastx.14	Pf 2= basic proline-rich protein(PRBI precursor 1 1 [Homo sapiens])	gi 386433 gb AAB27289.1	37% 53% 35% 40% 28% 40% 36% 36% 41% 41% 32% 33% 36% 36% 71% 71% 35%		158 62 325 133 158 133 225 225 74 74 325 158 158 183 44 44 74	271 242 59 63 63 59 160 160 24 24 242 87 93 118 24 24 24
HCUBJ11	967484	478	blastx.14						97
HCUDT65	915742	548	HMMER 2.1.1	PFAM: tRNA synthetases class II (A)	PF01411	35.1		697	930
			blastx.14	ORF YNL040w [Saccharomyces cerevisiae]	gi 1301892 emb CAA95907.1	42% 52% 31% 42%		763 658 1153 1678	972 759 1293 1740

HCUEU10	964857	595	HMMER 1.8		PFAM: Bacterial regulatory proteins, luxR family	PF00196		21%	1009	1149
HCUGB48	880730	647	HMMER 1.8		PFAM: TNFR/NGFR cysteine-rich region	PF00020		20%	1273	1494
HCUGR38	706471	670	HMMER 1.8		PFAM: Alcohol/other dehydrogenases, short chain type	PF00106		5.43	13	42
HCUHM44	615198	702	HMMER 1.8		PFAM: HMG (high mobility group) box	PF00505		7.99	173	226
HCWAK80	702435	748	HMMER 1.8		PFAM: Src homology domain 3	PF00018		73.02	102	284
HCWAR05	932623	759	blastx.14		hypothetical protein [Synechocystis sp.]	gi 1653272 dbj BAA1 8187.1		4.81	2	73
HCWBB63	667283	782	HMMER 2.1.1		PFAM: Secretory protein of YscJ/FliF family	PF01514		3.55	316	387
HCWBE76	968515	799	HMMER 1.8		PFAM: Helix-loop-helix DNA-binding domain	PF00010		47%	235	83
HCWBI37	967717	809	blastx.14		URF (pot. 4.5S protein) [Escherichia coli]	gi 42759 emb CAA25 537.1		46%	70	32
HCWBI53	934909	810	blastx.14		lepA [Mycobacterium tuberculosis]	gi 1655655 emb CAB 03723.1		71%	321	301
HCWBI90	921653	812	blastx.14		xylose isomerase [Klebsiella pneumoniae]	gi 43952 emb CAA43 389.1		78.2	45	275
HCWBN06	924638	825	blastx.14		collagen type XVII [Mus musculus]	gi 309183 gb AAA37 443.1		9.77	13	51
								63%	9	179
								85%	202	222
								60%	228	257
								85%	65	166
								84%	9	65
								59%	316	8
								55%	344	291
								26%	153	266
								46%	262	306

HCWBQ03	920886	834	blastx.14	ORF YBR208c [Saccharomyces cerevisiae]	gi 536588 emb CAA85172.1	57% 36% 46% 43% 75% 42%	5 75 259 310 337 78	46 140 303 357 360 119
HCWCM65	529230	891	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	69.62	31	264
HCWCR31	693632	909	HMMER 2.1.1	PFAM: ATP synthase (E/31 kDa) subunit	PF01991	80	229	381
HCWDI64	924632	945	blastx.14	tetracycline transporter-like protein [Mus musculus]	gi 2506078 dbj BAA22622.1	82% 87%	117 73	167 120
HCWDJ23	527555	952	HMMER 2.1.1	PFAM: Bacterial extracellular solute-binding proteins, family 3	PF00497	27.3	25	198
HCWDL45	889416	957	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.63	121	168
HCWDR01	839104	973	HMMER 1.8	PFAM: ABC transporters	PF00005	62.98	15	179
			blastx.2	(AE000411) putative ATP-binding component of a transport system [Escherichia coli]	gb AAC76377.1	69% 44% 51% 41%	9 18 281 391	215 200 373 477
HCWDV17	974478	993	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	81.59	416	613
HCWDX22	967361	1014	blastx.14	copC peptide	gi 151190 gb AAA25	79%	365	84

HCWDX76	932614	1019	blastx.14	[Pseudomonas syringae] (AF102543) unknown [Zymomonas mobilis]	808.1  gi 4378174 gb AAD1 9419.1	81%	423	358
HCWED61	971865	1041	blastx.14	gp210 (AA 1-1886) [Rattus norvegicus]	gi 56463 emb CAA68 759.1	75%	481	212
HCWEG69	948693	1058	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain.	PF00099	2.79	57	98
HCWEI19	948690	1066	blastx.14	orf3 [Pseudomonas aeruginosa]	gi 557259 emb CAA5 7572.1	55%	248	45
			HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	87%	56	9
			blastx.14	formaldehyde dehydrogenase (glutathione) [Escherichia coli]	gi 887431 emb CAA5 2057.1	8.6	226	273
HCWEL01	916972	1086	blastx.14	(AF010496) exonuclease SbcD homolog [Rhodobacter capsulatus]	gi 3128267 gb AAC1 6119.1	75%	300	10
HCWEM51	920887	1096	blastx.14	argininosuccinate lyase [Bacillus subtilis]	gi 2635409 emb CAB 14904.1	39%	34	171
			HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	47%	193	249
HCWEQ14	908245	1105	HMMER 1.8	(AC002985) R27090_2 [Homo sapiens]	gi 2443870 gb AAB8 1544.1	54%	365	39
HCWEW45	571355	1116	blastx.14	PFAM: Heat shock hsp90 proteins	PF00183	47%	57	7
			HMMER 1.8	(AJ000758) precorrin-4 methylase [Bacillus megaterium]	gi 3724045 emb CAA 04314.1	72.08	37	177
HCWEY34	954142	1125	blastx.14			100%	37	177
						66%	5	40
						10.32	37	186
						32%	3	242



HCWFF88	506577	1143	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.92	140	181
HCWFK57	861907	1149	HMMER 2.1.1	PFAM: RNA polymerase beta subunit	PF00562	36.2	34	270
HCWFT29	690751	1186	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	4.51	105	152
HCWUF66	853005	1196	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	71.4	105	269
HCWGB78	861843	1217	HMMER 2.1.1	PFAM: Ribosomal protein L31	PF01197	50.8	126	236
HCWGE12	967067	1223	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	4.04	214	288
HCWGW12	964088	1262	blastx.14	L-lactate dehydrogenase (EC 1.1.1.27) - Acinetobacter 1	pir A37334 A37334	73%	137	60
HCWGY90	960159	1288	HMMER 1.8	PFAM: Bacterial regulatory helix-loop- helix proteins, araC family	PF00165	58.7	6	137
			blastx.14	operon regulatory protein [Erwinia carotovora]	gi 148382 gb AAA24 811.1	86%	6	158
HCWHB12	970688	1295	blastx.14	Nodulation protein V (EC 2.7.3.-). [Escherichia coli]	gi 1736771 dbj BAA1 5920.1	47%	195	314
						33%	59	211
						85%	310	330
HCWHD07	953384	1305	blastx.14	Isp42p [Saccharomyces cerevisiae]	gi 736300 emb CAA8 8644.1	41%	56	301
						46%	298	393
						50%	341	394
HCWHP74	598510	1334	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.09	68	112

HCWHQ03	924187	1336	blastx.14	(AL049608) extensin-like protein [Arabidopsis thaliana]	gi 4584539 emb CAB40769.1	50%	85	14
HCWHQ31	574945	1337	HMMER 2.1.1	PFAM: Carbon-nitrogen hydrolase	PF00795	39.4	141	308
HCWHR81	935419	1343	HMMER 2.1.1	PFAM: Ribosomal protein L30p/L7e	PF00327	90.5	107	265
HCWHT59	924105	1349	blastx.14	(AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae]	gi 3510629 gb AAC80285.1	57%	261	148
						45%	327	148
						50%	261	148
						50%	261	148
						36%	122	9
						34%	122	9
						61%	329	252
						55%	157	104
						40%	104	9
						33%	107	9
						66%	142	107
						55%	305	252
						26%	249	160
						26%	249	160
						44%	305	252
						41%	157	107
						41%	157	107
						33%	311	249
						22%	107	15
						32%	246	163
HCWK08	959388	1388	blastx.14	pot. ORF I [Homo]	gi 1335196 emb CAA	57%	83	27

					sapiens]	26917.1	62%	303	256
HCWKN08	959380	1409	blastx.14		CeoB [Burkholderia cepacia]	gi 2109271 gb AAB58161.1	32% 47%	192 247	82 179
HCWKV68	959801	1427	blastx.14		(AL121600) hypothetical protein SCF76.09 1	gi 6002364 emb CAB56729.1	55% 50% 62% 54%	249 148 281 61	169 83 258 29
HCWLD06	935392	1437	blastx.14		ORF_o485 [Escherichia coli]	gi 887832 gb AAA83063.1	34% 42% 57%	219 120 238	142 43 218
HCWLE37	960093	1442	blastx.14		(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]	gi 4104812 gb AAD11957.1	47% 42% 35%	240 449 66	7 282 7
HCWLH79	959458	1453	blastx.14		(AC004877) sco-spondin-mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC36301.1	100% 85% 87% 44% 36%	126 304 103 66 250	263 345 126 119 315
HCWTB11	965024	1462	blastx.14		DNA primase [Escherichia coli]	gi 147755 gb AAA24600.1	27% 71%	289 326	191 306
HCWTB56	853009	1470	HMMER 1.8		PFAM: E1-E2 ATPases	PF00122	45%	341	3
			blastx.2		cadmium resistance protein [Lactococcus lactis]	gb AAB37345.1	55.15	2	301
							42%	2	316
HCWTR08	958791	1516	blastx.14		(AE000888) malate dehydrogenase [Methanobacterium	gi 2622314 gb AAB85694.1	43% 44%	66 182	134 262

HCWTR54	729290	1517	HMME 1.8	thermoautotrophicum] PFAM: Helicases conserved C-terminal domain	PF00271	6.14	151	198
HCWTS15	654317	1519	HMME 1.8	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	47.52	2	166
HCWU16	661570	1593	HMME 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.17	33	77
HDDMA83	926991	1633	blastx.14	(AF038963) RNA helicase [Homo sapiens]	gi 4405795 gb AAD1 9826.1	100% 51% 100% 90%	2 537 656 526	514 635 694 558
HDMAQ15	941282	1646	HMME 2.1.1	PFAM: POT family	PF00854	77.2	811	386
HDPAG32	947832	1655	blastx.2 2.1.1	(AF121080) cAMP inducible 1 protein [Mus musculus]	gb AAD24570.1 AF1 21080_1	80%	2	997
HDPCN94	794275	1678	HMME 2.1.1	PFAM: Peptidase family M1	PF01433	39.1	335	577
HDPFF07	974494	1694	blastx.14	PFAM: RhoGEF domain	PF00621	54.2	363	740
HDPIT53	926498	1736	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1	92% 96% 50%	513 715 458	716 789 505
HDPIT61	741724	1737	blastx.2	(AF109719) BAT2 [Mus musculus]	gi 3941737 gb AAC8 2480.1	50% 30%	229 278	170 219
				(AF121080) cAMP inducible 1 protein [Mus musculus]	gb AAD24570.1 AF1 21080_1	73% 57%	48 293	329 397

HDPKD52	959653	1750	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041	4.82	340	402
HDPLC45	909091	1755	HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651	39.5	280	507
HDPMA48	582015	1775	blastx.2	(AF038007) FIC1 [Homo sapiens]	gb AAC63461.1	54%	152	703
HDPMO62	912722	1780	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	132.39	127	432
			blastx.2	rab-related GTP-binding protein [Homo sapiens]	emb CAA68227.1	54% 57%	133 20	444 76
HDPNC96	934520	1788	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	206.63	3	734
			blastx.14	HUMAN NDR [unidentified]	gi 2304746 emb CAA 03387.1	92%	3	734
HDPOJ93	792193	1797	HMMER 1.8	PFAM: EF hand	PF00036	7.78	266	313
HDPPP24	812091	1815	HMMER 2.1.1	PFAM: Fes/CIP4 homology domain	PF00611	22.4	151	387
HDPPU44	951276	1818	HMMER 1.8	PFAM: Lectin C-type domain short and long forms	PF00059	37.49	245	376
HDPRH02	919404	1837	blastx.14	ORF YGR090w [Saccharomyces cerevisiae]	gi 1323133 emb CAA 97093.1	30% 48%	266 593	451 673
			blastx.14	reverse transcriptase [Homo sapiens]	gi 439877 gb AAB02 291.1	66% 37% 54%	6 280 235	59 351 267
HDPTW90	722699	1868	HMMER 1.8	PFAM: IG (immunoglobulin)	PF00047	3.32	1	24

HDPVG11	966556	1877	HMMER-1.8	superfamily PFAM: PH (pleckstrin homology) domain	PF00169	16	518	613
HDPWE80	909916	1890	HMMER-2.1.1	PFAM: PH domain	PF00169	81.2	412	708
			blastx.2	(AF102854) membrane-associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus]	gb AAD04568.1	36%	349	756
HDPWY46	915964	1894	blastx.14	(AF061738) leucine aminopeptidase [Homo sapiens]	gi 4335941 gb AAD17527.1	94% 87% 80% 95% 62% 33%	3 316 140 254 425 305	152 438 217 316 472 358
HDQEF04	927024	1914	blastx.14	Bassoon [Mus musculus]	gi 3413810 emb CAA76598.1	75%	239	216
HDQGT70	909848	1936	blastx.14	Bat2 [Homo sapiens]	gi 29375 emb CAA78744.1	37%	248	201
HDQHT10	963481	1944	blastx.14	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]	gi 4104812 gb AAD11957.1	58% 43% 100% 55% 42% 58% 83%	490 387 76 253 256 45 51	455 319 59 227 215 10 34
HDQHZ10	961336	1945	blastx.14	fractionated X-irradiation-induced 29 thymoma [Mus musculus]	gi 1389694 gb AAB02905.1	51% 71%	47 2	256 43
HDQHZ22	879416	1946	blastx.2	cysteine rich hair keratin	emb CAA56339.1	40%	65	319

					associated protein [Oryctolagus cuniculus] (AF086624) serine threonine kinase [Rattus norvegicus]		42%	65	352
HDTAY23	973925	1956	blastx.14			gi 3800869 gb AAC6 8900.1	98%	78	254
HDTAY23	974565	9561	blastx.14		(AF086624) serine threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6 8900.1	98% 85% 100% 66%	79 330 371 305	255 371 403 331
HDTBO48	945083	1959	HMMER 1.8		PFAM: IG (immunoglobulin) superfamily	PF00047	18.53	159	347
			blastx		(AJ009698) embigin protein [Rattus norvegicus]	emb CAA08796.1	58% 75% 58%	132 273 357	248 356 464
HDTBR50	846630	1968	HMMER 1.8		PFAM: Thioredoxins	PF00085	29.85	163	297
HDTBY88	934472	1973	HMMER 2.1.1		PFAM: Eukaryotic protein kinase domain	PF00069	93.6	3	302
			blastx.14		p56 KKIAMRE protein kinase [Homo sapiens]	gi 1517820 gb AAC5 0918.1	82% 35% 100%	3 192 492	170 458 509
HDITDC53	916348	1977	HMMER 1.8		PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.98	180	233
HDTEI19	912765	1984	blastx.14		rab4b [Canis familiaris]	gi 919 emb CAA3980 0.1	78% 88%	244 387	354 413
HDTES50	964709	1987	HMMER 1.8		PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076	31.58	108	326
			blastx.2		arginine-rich nuclear	gb AAA35554.1	65%	36	350

HDTHQ15	923899	2009	blastx.14	protein [Homo sapiens] Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) [Homo sapiens]	gi 1665781 dbj BAA1 3387.1	97%	4	612
HDTHZ46	957669	2012	blastx.14	(AC004877) sco-spondin- mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC3 6301.1	43% 42% 46% 43% 40% 38%	100 45 172 2 5 318	168 101 216 49 49 371
HDTID61	908946	2016	HMMER 1.8 blastx.2	PFAM: Zinc finger, C2H2 type (AK002053) unnamed protein product [Homo sapiens]	PF00096 dbj BAA92059.1	7.07 46% 53% 50% 45% 47% 49% 46% 33% 42% 34% 51% 57% 37% 32% 50% 47% 66%	407	430
HDTIF01	883070	2017	blastx.2	(AF010144) neuronal	gb AAC08737.1	61%	315	524



					thread protein AD7c-NTP [Homo sapiens]				61%	309	509
									65%	361	507
									62%	34	162
									60%	53	172
									41%	304	507
									35%	286	507
									40%	327	473
									50%	50	151
									57%	89	166
									47%	109	171
									37%	308	379
									52%	128	178
HDTIZ44	925574	2032	blastx.14	procollagen alpha 2(V) [Homo sapiens]	gi 2370202 emb CAA 75002.1				43%	77	9
									40%	89	9
									37%	89	9
									57%	229	188
									47%	183	133
									60%	135	106
									47%	328	278
									75%	165	142
									60%	121	92
									43%	139	92
									54%	165	133
									60%	162	133
									54%	226	194
HDTJI37	799834	2036	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052				2.02	386	466
HDTJJ02	913787	2037	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130				5.7	21	68
HDTKQ14	886936	2044	HMMER	PFAM: Src homology	PF00018				12.87	430	546

HDTLD17	908601	2052	1.8	domain 3	emb CAB41255.1			
			blastx.2	(AL049683) hypothetical protein [Homo sapiens]		100%	439	555
			HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	56%	76	291
			blastx.2	Zfp-29 [Mus musculus]	emb CAA38920.1	96.3	154	222
						48%	49	636
						65%	49	399
						66%	49	399
						66%	70	399
						65%	49	411
						62%	49	369
						64%	70	381
						47%	115	636
						58%	49	324
						42%	372	641
						50%	375	569
						47%	375	569
						47%	375	569
						48%	372	569
						43%	372	578
						42%	372	602
						46%	375	569
						35%	279	569
						43%	372	569
						43%	375	569
						46%	375	569
						63%	547	636
						63%	547	636
						52%	538	651
						56%	547	642
						35%	375	491

HEOMG48	963338	2091	blastx.14	very large tegument protein [human herpesvirus 2]	gi 1869859 emb CAB06722.1	66%	641	667
HEOMG78	920911	2092	blastx.14	contains similarity to C2 domains [Caenorhabditis elegans]	gi 1825586 gb AAB42222.1	70% 40%	294 136	437 246
HEOMS08	959581	2113	blastx.14	(AF034970) docking protein [Homo sapiens]	gi 3043919 gb AAC13265.1	93% 83%	129 172	173 207
HEOMT79	936687	2118	blastx.14	(AF108420) 1-aminocyclopropane-carboxylate synthase [Fugu rubripes]	gi 4426837 gb AAD20564.1	52%	10	210
HEOMU79	965900	2121	blastx.14	HLA-B-associated transcript 2 (BAT2) [Homo sapiens]	gi 179339 gb AAA35585.1	29%	320	198
HEOMX92	919200	2131	blastx.14	TGR-CL5bis [Homo sapiens]	gi 1247469 emb CAA01862.1	53% 38% 53% 30% 27%	274 129 271 44 206	230 91 233 6 174
HEOMX92	961148	9562	blastx.14	retrovirus-related reverse transcriptase pseudogene - slow loris	pir B25313 GNLRL1	46% 50%	44 247	241 312
HEONQ19	930705	2142	HMMER 2.1.1	PFAM: PH domain	PF00169	42.5	213	533
			blastx.2	(AJ250425) Collybistin I [Rattus norvegicus]	emb CAB65966.1	96%	9	629

HEONV59	949152	2148	blastx.2	(AK001463) unnamed protein product [Homo sapiens]	dbj BAA91707.1	51%	163	279
HEOPE58	851009	2157	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.32	320	364
HEOPO08	958184	2174	blastx.14	alpha-1 type II collagen [Xenopus laevis]	gi 214044 gb AAA49679.1	38%	142	11
						32%	429	346
						31%	429	334
						75%	273	250
						36%	208	134
HEOQC76	909032	2189	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	86.9	169	237
			blastx.2	(AK001753) unnamed protein product [Homo sapiens]	dbj BAA91884.1	37%	139	609
						33%	139	609
						35%	139	480
						52%	154	306
						29%	196	582
HEOQP44	942596	2203	HMMER 2.1.1	PFAM: Beta-lactamase	PF00144	420.7	250	1026
HEOQS11	965930	2204	blastx.14	ORF1A [Homo sapiens]	gi 475909 emb CAA47472.1	51%	30	152
HEORE79	959572	2214	blastx.14	rehydrin [Tortula ruralis]	gi 1732471 gb AAB49656.1	53%	101	145
						46%	101	145
						50%	232	267
						50%	284	325
						55%	58	84
						55%	180	206
						42%	223	264
						62%	58	81
						62%	180	203
						62%	302	325

HHECO01	915285	2250	blastx.14	(AF039691) antigen NY-CO-9 [Homo sapiens]	gi 3170182 gb AAC18040.1	65%	302	174
HHEEC07	952455	2267	blastx.14	(AF064257) Dhml-like protein [Homo sapiens]	gi 5881961 gb AAD55138.1 AF064257 1	100%	25	2
HHEHU73	923895	2279	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	99%	1202	1801
						100%	1862	1912
HHEJH30	961974	2282	blastx.14	(AF180920) cyclin ania-6a [Homo sapiens]	gi 5823554 gb AAD53184.1 AF180920 1	4.1	115	156
HHEND45	919630	2302	HMMER 1.8	PFAM: Double-stranded RNA binding motif	PF00035	95%	226	417
			blastx.14	[D.melanogaster mRNA, complete cds.], gene product [Drosophila melanogaster]	gi 158506 gb AAA73062.1	95%	429	494
						12.86	25	114
HHEQK01	871911	2346	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	52%	1	114
						47%	235	297
HHEQV39	932851	2354	HMMER 1.8	PFAM: Src homology domain 3	PF00018	3.27	64	90
HHESU85	783820	2381	HMMER 1.8	PFAM: Heat shock hsp90 proteins	PF00183	30.41	526	708
HHETQ54	908567	2392	HMMER 2.1.1	PFAM: KRAB box	PF01352	11.81	88	288
			blastx.14	NK10 [Mus musculus]	gi 506502 emb CAA56225.1	166.4	233	421
						89%	212	448
HHEUA62	965709	2400	HMMER 1.8	PFAM: Spectrin alpha chain, repeated domain	PF00435	10.48	103	186
			blastx.14	(AB023622) Septin6 [Mus musculus]	gi 5689158 dbj BAA82838.1	59%	13	144
						60%	211	315

HHEUC31	795268	2401	HMMER 2.1.1	PFAM: Ank repeat	PF00023	31.5	3	92
HKBAT27	963724	2486	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.17	11	37
HLMBW11	950728	2526	blastx.14	(AF156884) RIP-like kinase [Homo sapiens]	gi 5059425 gb AAD3 9005.1 AF156884_1	92%	129	782
HLMBY16	531053	2529	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	1.99	82	123
HLMDU71	531228	2572	HMMER 2.1.1	PFAM: Phosphate- binding protein	PF01449	48.1	1	123
HLMFU09	909666	2600	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1	78%	277	372
HLMHP67	967636	2633	blastx.14	Hypothetical bacteriophage n4 receptor protein NfrA precursor. [Escherichia coli]	gi 1651236 dbj BAA3 5202.1	82% 100%	107 3	340 104
HLMHT94	531054	2641	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.86	264	284
HLMIX95	960056	2679	blastx.14	(AB008430) CDEP [Homo sapiens]	gi 2766165 dbj BAA2 4267.1	89% 69%	440 47	330 9
HLMMA52	920292	2694	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47 471.1	43% 100% 70%	115 165 174	162 176 203
HLMMD05	932127	2697	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1	50% 61% 44% 58% 63% 50%	189 355 189 107 349 387	124 317 115 72 317 352

								42%	358	317
								50%	407	366
								46%	355	317
								46%	110	66
								32%	189	115
								46%	355	317
HLMNV66	926188	2733	HMMER 1.8	PFAM: Ank repeat			PF00023	17.86	245	322
			blastx.14	similar to HUMORFU (D26069) [Homo sapiens]			gi 488505 dbj BAA06 418.1	62%	230	382
								81%	337	384
								86%	404	448
								71%	378	419
								39%	173	256
								43%	99	146
HLMNL55	964739	2769	blastx.14	dynein heavy chain isotype 6 [Tripneustes gratilla]			gi 687206 gb AAA63 589.1	70%	19	138
								37%	184	231
HLMNN02	920296	2776	blastx.14	(AF083501) latent nuclear antigen [Macaca mulatta rhadinovirus 17577]			gi 4494984 gb AAD2 1406.1	36%	345	289
								53%	191	153
								50%	86	57
								33%	306	208
HL YAA41	909874	2871	HMMER 2.1.1	PFAM: PH domain			PF00169	37.3	162	260
HL YDL60	909866	2980	blastx.14	ORF-3 protein [Pseudorabies virus]			gi 334072 gb AAA47 471.1	44%	89	15
								37%	229	158
								35%	376	293
								30%	259	191
								39%	283	215
								75%	179	156
								47%	232	182
								75%	26	3

HL YDS11	966732	2986	blastx.14	orfIV [Borna disease virus]		gi 473842 gb AAA20666.1	38%	250	197
HL YDT68	526245	2991	HMMER 1.8	PFAM: Zinc finger, C2H2 type		PF00096	39%	200	161
HL YDV62	927872	2993	HMMER 2.1.1	PFAM: PH domain		PF00169	4.11	89	124
			blastx.2	(AC005496) unknown protein [Arabidopsis thaliana]		gb AAC35236.1	41%	113	292
HL YEN93	682176	3005	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain		PF00130	38%	451	504
HL YGP46	832311	3042	HMMER 2.1.1	PFAM: IQ calmodulin-binding motif		PF00612	2.86	383	409
HL YHN67	920551	3056	blastx.14	EDTP(egg derived tyrosine phosphatase).		sp BAA33720 BAA33720	24.4	12	74
HMAAF10	968199	3062	blastx.14	Formate c-acetyltransferase (EC 2.3.1.54). [Escherichia coli]		gi 1651427 dbj BAA35638.1	65%	1	234
							47%	264	314
							100%	1	300
							76%	347	385
HMABJ56	907640	3063	HMMER 2.1.1	PFAM: ADP-ribosylation factor family		PF00025	24.8	157	231
			blastx.14	(AF082517) ADP-ribosylation factor [Entamoeba histolytica]		gi 3746799 gb AAC64063.1	39%	281	403
							56%	154	228
							61%	233	271
HMABQ71	729831	3065	HMMER 2.1.1	PFAM: DNA topoisomerase II (N-terminal region)		PF00204	128.8	210	407



HMADC02	920088	3067	blastx.14	ORF_f418 [Escherichia coli]	gi 536985 gb AAA97040.1	95%	202	143
HMAZD55	939916	3071	blastx.2	(AK002022) unnamed protein product [Homo sapiens]	dbj BAA92041.1	98%	270	728
HMAFY42	778521	3078	HMMER 2.1.1	PFAM: WH1 domain	PF00568	90	46	303
HMAAGK69	723186	3080	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	40.87	31	405
HMAIC22	947905	3085	HMMER 2.1.1	PFAM: Peptidase family M3	PF01432	65.9	115	402
HMAKA11	966282	9569	blastx.14	CG Site No. 18031 [Escherichia coli]	gi 466635 gb AAB18474.1	84%	112	390
						100%	2	112
						55%	363	422
HMAKA11	966282	9569	blastx.14	MaoB [Escherichia coli]	gi 1480003 dbj BAA11058.1	99%	1516	803
						90%	1673	1545
						50%	1587	1474
HMAALL66	956195	3091	HMMER 1.8	PFAM: Adenylate kinases	PF00406	50.17	63	296
HMCDN22	895981	3107	blastx.2	(AJ007798) stromal antigen 3, (STAG3) [Homo sapiens]	emb CAB59367.1	82%	85	456
						90%	445	573
HMCFB22	963794	3110	blastx.14	probable transposase - human transposon MER37	pir S72481 S72481	71%	10	168
						73%	183	320
						82%	119	187
HMCY77	753133	3117	HMMER 2.1.1	PFAM: Kelch motif	PF01344	43%	313	423
						61%	5	58
						63%	90	122
HMMAB49	462502	3127	HMMER	PFAM: Zinc-binding	PF00099	51.9	7	132
						3.49	166	183

HMMAC19	953580	3129	1.8 blastx.14	metalloprotease domain (AF003535) ORF2-like protein [Homo sapiens]	gi 2197085 gb AAD0 4635.1	47%	26	145
HMMCH04	944069	3208	blastx.2	unknown [Homo sapiens]	gb AAC50940.1	58%	423	680
HMQBU96	765162	3247	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	7.33	8	40
HMQDZ19	940694	3267	blastx.14	urokinase plasminogen activator receptor [Homo sapiens]	gi 433901 emb CAA5 2191.1	100% 91%	89 133	124 168
HMSBV28	970579	3303	blastx.14	YKL249 [Saccharomyces cerevisiae]	gi 871536 emb CAA4 9304.1	92% 51% 50%	260 141 323	108 1 282
HMSCD15	918133	3310	HMMER 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
			blastx.2	(AK000975) unnamed protein product [Homo sapiens]	dbj BAA91451.1	98% 29% 28%	453 387 80	635 479 175
HMSFR69	738588	3373	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.78	258	202
HMSGGL27	855759	9573	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	5.56	276	202
HMSGP73	925385	3401	blastx.14	(AC004490) R29381_1 [Homo sapiens]	gi 2995577 gb AAC0 8316.1	94% 95%	141 901	908 972
HMSGX14	871492	3413	HMMER 1.8	PFAM: Ribosomal protein S12	PF00164	33.44	28	153
HMSHO64	746582	3431	HMMER 1.8	PFAM: Src homology domain 3	PF00018	11.08	316	405
			blastx.2	(AF030131) Plenty of SH3s; POSH [Mus]	gb AAC40070.1	47%	1	411

HMSHZ56	733386	3447	HMMER 1.8	musculus] PFAM: Zinc finger, CCHC class	PF00098	4.89	208	228
HMSJT11	965007	3491	blastx.14	(AF148805) latent nuclear antigen [Kaposi sarcoma- associated herpesvirus]	gi 5669894 gb AAD4 6501.1 AF148805_6	20% 24% 21% 23% 16%	667 241 241 211 139	1137 465 465 453 465
HMSJW19	744990	3498	HMMER 2.1.1	PFAM: BAH domain	PF01426	48.7	2	163
HMSKI08	959413	3509	blastx.14	(AF094516) E1-like protein [Homo sapiens]	gi 3820614 gb AAC6 9630.1	97%	97	513
HMSOM08	958216	3538	blastx.14	(AF082556) TRF1- interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	gi 3929219 gb AAC7 9841.1	76%	2	232
HMSOU92	948130	9578	blastx.2	(AF118082) PRO1902 [Homo sapiens]	gb AAF22026.1 AF1 18094_21	64% 63% 88%	302 462 532	463 527 558
HMSOX47	948202	3548	blastx.14	cDNA EST EMBL:M89462 comes from this gene; cDNA EST 1 1 yk349d7.5 comes from this gene; cDNA EST yk358b9.5 comes from this	gi 3879085 emb CAA 94301.1	48% 39% 36% 39% 26%	514 365 266 173 514	612 463 355 256 591
HMVVDU16	904807	3589	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	13.38	1252	1329
HMWCCQ09	924634	3606	blastx.14	Emf1 alpha [Ephydatia muelleri]	gi 9300 emb CAA494 72.1	50% 33% 66%	19 99 217	84 233 243

HMWDD54	932261	3610	blastx.14	(AF175223) SANT domain protein SMRTER [Drosophila melanogaster]	gi 5815245 gb AAD52614.1 AF175223_1	38%	292	345
HMWDF88	906769	3612	HMMER 1.8	PFAM: Low-density lipoprotein receptor domain class A	PF00057	41.61	171	245
			blastx.14	(AF110520) NG29 [Mus musculus]	gi 4050096 gb AAC97969.1	69%	114	239
						48%	129	239
						35%	9	110
						50%	72	107
HMWGG55	920575	3642	blastx.14	DNA polymerase [Pyrococcus furiosus]	gi 216918 dbj BAA02362.1	94%	195	308
HMWGT07	953454	3645	blastx.14	(AL078579) putative protein [Arabidopsis thaliana]	gi 4972120 emb CAB43977.1	40%	218	322
						40%	395	475
						46%	113	157
HMWHN70	851334	3654	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	6.51	187	255
HNEBJ08	958742	3689	blastx.14	mucin 2 precursor, intestinal - human (fragments)	pir A49963 A43932	35%	305	264
						83%	320	303
HNEDU01	909832	3748	blastx.14	(AC002398) F25965_3 [Homo sapiens]	gi 2477513 gb AAB81198.1	71%	207	323
						57%	80	205
						62%	1	87
						43%	323	412
						50%	337	384
HNFEF95	971171	3792	blastx.14	ORF_o493 [Escherichia coli]	gi 606260 gb AAA58123.1	98%	548	201
						89%	103	20
						81%	185	105
HNFFM25	705856	3818	HMMER	PFAM: Laminin B	PF00052	0.47	520	603

HNFFT62	574623	3828	1.8	(Domain IV) PFAM: C2 domain	PF00168	2.74	207	272
HNFGI01	921431	3851	blastx.14 1.8	(AF118890) s-tomosyn isoform [Rattus norvegicus]	gi 4689231 gb AAD2 7819.1 AF118890_1	86% 100% 40%	234 153 287	302 200 361
HNFGI49	909707	3852	blastx.14	(AF086624) serine threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6 8900.1	100% 100%	1 60	45 86
HNFGM76	908665	3862	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	74.8	232	306
			blastx.2	(AF132599) RANTES factor of late activated T lymphocytes-1 [Homo sapiens]	gb AAD26864.1 AF1 32599_1	92%	1	417
HNFHA11	967520	3874	HMMER 2.1.1	PFAM: Phosphoenolpyruvate carboxykinase	PF01293	118.1	55	219
			blastx.14	phosphoenolpyruvate carboxykinase [Escherichia coli]	gi 606337 gb AAA58 200.1	99%	55	360
HNFBK77	576186	3890	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	30.2	231	326
HNFBQ01	938114	3897	blastx.14	serine/threonine kinase with SH3 domain, leucine 1	gi 758593 emb CAA8 8531.1	28% 46% 46% 25% 41%	248 43 371 79 176	331 81 415 186 211
HNFBW14	939763	3908	HMMER 2.1.1	PFAM: Latrophilin/CL-1- like GPS domain	PF01825	35.1	44	196

				blastx.2	(AF166382) serpentine receptor [Mus musculus]	gb AAF00617.1 AF166382_1	44%	38	283
HNFIF07	918389	3921	blastx.14		(AF128881) PI3 kinase regulatory subunit P101 [Homo sapiens]	gi 4928058 gb AAD33397.1 AF128881_1	80% 60%	2 448	445 477
HNFIF50	965283	3936	blastx.14		mutant sterol regulatory element binding protein-2 1	gi 841318 gb AAA85718.1	65% 34% 85%	356 42 665	631 128 685
HNGAL92	953889	3976	blastx.14		phosphatidylserine decarboxylase [Escherichia coli]	gi 551827 gb AAA83896.1	73%	212	18
HNGASS1	773208	3984	HMMER 1.8		PFAM: Zinc-binding metalloprotease domain	PF00099	2.57	144	182
HNGBF80	574475	4001	HMMER 1.8		PFAM: Zinc finger, C2H2 type	PF00096	4.98	88	111
HNGBH77	577361	4005	HMMER 1.8		PFAM: ATP synthase A chain	PF00119	9.81	130	189
HNGCE85	970738	4039	blastx.14		hypothetical protein Tigger 2 - human transposon MER37 1	pir S72489 S72489	72% 63%	284 212	210 180
HNGCX07	953900	4065	HMMER 1.8		PFAM: Src homology domain 3	PF00018	3.68	45	161
HNGEN37	663955	4160	HMMER 2.1.1		PFAM: Indole-3-glycerol phosphate synthases	PF00218	125.4	2	223
HNGEQ07	953647	4169	HMMER 1.8		PFAM: TPR Domain	PF00515	10.86	164	238
HNGER43	699391	4173	HMMER 1.8		PFAM: Bacterial mutT protein	PF00293	3.79	151	195
HNGER96	922996	4177	blastx.14		Bkm-like protein [Drosophila melanogaster]	gi 552132 gb AAA28872.1	60% 64%	250 250	294 291

HNGEW76	572874	4198	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	64%	250	291
HNGEX35	959230	4200	blastx.14	adenine phosphoribosyltransferase [Escherichia coli]	gi 1773151 gb AAB4 0223.1	75%	215	250
HNGEX95	572897	4202	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	80%	28	57
HNGFG22	573084	4224	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	4.66	194	247
HNGFG69	926873	4227	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1	98%	205	366
HNGFK28	544726	4234	HMMER 1.8	PFAM: ABC transporters	PF00005	5.32	196	219
HNGFK28	566798	9584	HMMER 1.8	MsbA protein. [Escherichia coli]	dbj BAA35658.1	9.2	166	240
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	44%	228	175
HNGFK28	943114	9585	HMMER 1.8	MsbA protein. [Escherichia coli]	dbj BAA35658.1	40%	145	80
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	40%	145	80
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	40%	307	248
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	50%	67	38
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	86.07	445	654
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	1	651
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	86%	654	989
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	86.07	445	654
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	1	651
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	654	989
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	117.67	342	1
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	165	503

HNGFK28	943115	9586	HMMER 2.1.1 blastx.2	[Escherichia coli] PFAM: ABC transporter transmembrane region. MsbA protein. [Escherichia coli]	PF00664 dbj BAA35658.1	84% 91% 60.9 99%	25 2 3 3	162 37 242 512
HNGFO46	935135	4244	blastx.14	hypothetical protein T23G5.2 - Caenorhabditis elegans	pir S28303 S28303	44% 60% 40% 36%	84 116 205 263	10 87 161 198
HNGFO81	526792	4246	HMMER 2.1.1	PFAM: Integrase core domain	PF00665	42.7	84	215
HNGFU12	971170	4265	HMMER 1.8 blastx.14	PFAM: RNase H reverse transcriptase (476 AA) [Woolly monkey sarcoma virus]	PF00075 gi 930259 emb CAA3 3367.1	55.68 44% 60%	102 96 1	290 422 75
			blastx.14	180 kDa bullous pemphigoid antigen 2/type XVII collagen [Homo sapiens]	gi 1877435 gb AAB5 1499.1	50% 53% 66% 36% 75% 60% 85% 85% 60% 54% 50% 26% 62% 75%	196 167 155 75 152 335 152 152 196 196 289 131 152 152	155 129 129 1 129 306 132 132 167 164 248 63 129 129
HNGFW09	924693	4270	blastx.14					



HNGGH78	924908	4306	blastx.14	type VII collagen [Cricetulus griseus]	gi 388625 gb AAA36 968.1	75% 66% 66% 60%	152 155 155 193	129 129 129 164
HNGGM10	964819	4317	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	50% 34% 42% 40% 50% 58% 38% 41% 50%	356 47 285 288 171 171 6 53 171	397 115 341 347 206 206 59 103 206
HNGGR74	765698	4340	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.36	14	58
HNGHT06	935706	4450	blastx.14	unknown protein [Homo sapiens]	gi 196398 gb AAA8 8020.1	50%	254	177
HNGIU01	916748	4483	blastx.14	ORF2 [Rattus norvegicus]	gi 56588 emb CAA37 645.1	50% 57% 57%	168 280 73	293 342 114
HNGKE07	952221	4630	blastx.14	collagen type VII [Homo sapiens]	gi 495866 gb AAA58 965.1	58% 55% 47% 64% 57% 32% 33% 62%	336 93 155 327 266 87 81 355	286 40 105 286 225 13 1 332
HNGLE52	835972	4662	HMMER	PFAM:	PF00049	6.75	286	318

				1.8	Insulin/IGF/Relaxin family				
HNGLG06	839088	4666		HMMER 1.8	PFAM: ABC transporters	PF00005	47.92	348	599
				blastx.2	Hypothetical protein HI0658 [Escherichia coli]	dbj BAA35501.1	99%	270	665
HNGLH82	954140	4668		blastx.14	diaminopimelate decarboxylase [Escherichia coli]	gi 455170 gb AAA83861.1	98%	416	249
							71%	193	47
HNHGM87	806036	4715		HMMER 1.8	PFAM: ATP synthase A chain	PF00119	63%	258	136
							8.41	237	362
HNGOO22	953888	4762		blastx.14	(AE000449) putative xylanase [Escherichia coli]	gi 1790156 gb AAC76742.1	94%	104	3
							91%	151	116
HNHAI11	967668	4790		blastx.14	p15E carboxyterminal sequence [Kirsten murine sarcoma virus]	gi 4469304 emb CAA25493.1	38%	262	161
							28%	406	323
HNHBE19	724404	4798		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	53%	310	272
							4.4	113	145
HNHBY45	774280	4823		HMMER 1.8	PFAM: ATP synthase A chain	PF00119	8.4	228	347
HNHDM74	506621	4878		HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	1.89	395	427
HNHDY50	924211	4910		blastx.14	unknown protein [Homo sapiens]	gi 196398 gb AAA88020.1	50%	33	170
							44%	23	169
HNHEJ85	964882	4955		blastx.14	synexin - bovine (fragment)	pir A27695 A27695	41%	6	164
							54%	47	15
							46%	91	53

HNHET25	953410	5002	blastx.14	(AJ005562) SPR2D protein [Mus musculus]	gi 3093363 emb CAA06591.1	40%	114	85
HNHFA11	967126	5030	blastx.14	(AF144054) apoptosis related protein APR-4 [Homo sapiens]	gi 4868437 gb AAD31316.1 AF144054_1	38%	91	53
HNHGD07	953416	5121	blastx.14	(AF053091) eyelid [Drosophila melanogaster]	gi 2981221 gb AAC06254.1	32%	347	246
HNHGE09	939727	5127	blastx.2	IDN4-GGTR14 PROTEIN.	sp Q9Y6Y5 Q9Y6Y5	43%	250	203
HNHGH20	959499	5146	blastx.14	notch4 [Homo sapiens]	gi 1841543 gb AAC63097.1	46%	207	169
HNHGV22	674653	5189	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	52%	212	355
HNHHI10	964659	5251	blastx.14	ORF1 [Rattus norvegicus]	gi 56587 emb CAA37644.1	35%	342	401
						46%	164	241
						55%	227	280
						33%	295	384
						30%	259	384
						50%	346	381
						36%	268	333
						26%	259	384
						62%	367	390
						42%	322	378
						62%	367	390
						83%	367	384
						81%	2	112
						43%	56	9
						77%	154	128
						33%	256	167
						33%	297	244
						62%	131	108
						4.66	94	138
						56%	75	28
						34%	157	71

HNHHL74	765598	5266	HMMER 1.8		PFAM: Bacterial mutT protein	PF00293		33%	220	158
HNHIA95	908419	5318	HMMER 2.1.1		PFAM: gag gene protein p24 (core nucleocapsid protein)	PF00607		63%	187	155
HNHPH29	934456	5496	blastx.14		(AF118275) atrophin- related protein ARP [Homo sapiens]	gi 4680231 gb AAD2 7584.1 AF118275_1		3.57	83	148
HOIAE91	935322	5497	HMMER 1.8		PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		67.6	49	300
HSATQ28	866951	5512	HMMER 1.8		PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442		60%	363	407
HSAYN79	471037	5646	HMMER 1.8		PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076		45%	14	73
HSYBL15	660053	5682	HMMER 1.8		PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		70%	91	120
HSYDP04	970789	5686	blastx.14		(AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]	gi 5106956 gb AAD3 9906.1 AF113615_1		50%	262	297
HT3SA07	954360	5702	blastx.14		ORF2 contains a reverse transcriptase domain.; ORF2 [Homo sapiens]	gi 339771 gb AAA51 622.1		47%	310	360
HT4GJ85	909971	5714	HMMER		PFAM: PH (pleckstrin domain)	PF00169		2.66	200	235
								11.1	90	122
								4.12	360	380
								22.31	2	70
								100%	77	394
								50%	408	467
								54%	393	443
								50%	83	178
								54%	47	79
								11.11	365	451

			1.8	homology) domain			
			blastx.14	(AF053974) SWAP-70 [Mus musculus]	gi 3290154 gb AAC4 0155.1	53%	251
HT5EA69	952359	5721	blastx.14	(AL032624) cDNA EST yk321h8.5 comes from this gene; 1 from this gene [Caenorhabditis elegans]	gi 3881086 emb CAA 21522.1	88% 33%	4 448
HTAAW46	719422	5735	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	37% 30%	264 123
HTABG87	940153	5745	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	5.82	6
			blastx.14	(AF006064) protein kinase homolog [Fowlpox virus]	gi 2393890 gb AAC5 8236.1	13.81	240
HTACW17	961560	5760	blastx.14	(AC007660) unknown protein [Arabidopsis thaliana]	gi 4895220 gb AAD3 2806.1 AC007660_7	54% 33%	8 189
HTAFE69	944409	5797	blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	37% 61%	54 212
HTAHL45	908949	5817	HMMER 2.1.1	PFAM: SCAN domain	PF02023	69%	432
			blastx.14	(AC004522) Zn-finger- like protein; similar to Z98745 (PID:g2924250) [Homo sapiens]	gi 3006231 gb AAC0 9486.1	228.7	268
HTAHV04	926747	5826	blastx.14	(AC005757) R32611_1 [Homo sapiens]	gi 3688089 gb AAC6 2258.1	65% 36%	220 529
HTAJN08	958057	5841	HMMER	PFAM: Helicases	PF00271	100%	3
						5.49	20
							55

				1.8	conserved C-terminal domain				
HTDAE43	971582	9597		blastx.14	(AF144054) apoptosis related protein APR-4 [Homo sapiens]	gi 4868437 gb AAD31316.1 AF144054_1	53%	526	296
HTGCH58	909849	5895		HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	91.4	420	797
				blastx.14	carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene	gi 3874826 emb CAA86318.1	37% 44% 61%	420 657 771	605 758 809
HTGDM65	967158	5918		blastx.14	SH3 domain binding protein [Rattus norvegicus]	gi 1185397 gb AAA87791.1	39% 50% 39% 47% 39% 28% 40%	127 186 278 186 278 337 260	59 139 210 136 210 263 195
				HMMER 2.1.1	PFAM: SpoU rRNA Methylase family	PF00588	107.6	315	638
HTGDT91	974962	5921		blastx.14	alternate gene name yibK [Escherichia coli]	gi 466744 gb AAB18583.1	100% 100% 76% 81%	315 531 457 497	467 638 495 529
				HMMER 2.1.1	PFAM: Domain of unknown function	PF01784	130.2	334	711
HTGDW96	967030	5926		blastx.14	(AL034490) similar to yeast ngg1-interacting factor 3	gi 4008560 emb CAA22481.1	60% 43% 37%	1087 460 385	1275 660 513

HTGEL46	685425	5936	HMMER 1.8	[Schizosaccharomyces pombe]		61%	361	414
				PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	28%	970	1065
						58%	1312	1347
HTGEQ11	967047	5944	HMMER 2.1.1 blastx.14	PFAM: Cytosol aminopeptidase family aminopeptidase A [Escherichia coli]	PF00883 gi 1054725 emb CAA 60164.1	7.26	398	433
						191	27	305
HTGER72	683469	5949	HMMER 1.8	PFAM: Src homology domain 3	PF00018	95%	27	305
						83%	320	391
HTGFZ03	923443	5968	HMMER 2.1.1 blastx.14	PFAM: RNA polymerase beta subunit (AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus]	PF00562 gi 2739048 gb AAB9 4600.1	88%	1	27
						2.4	174	203
HTGGL23	974590	5973	blastx.14	(AE000218) putative adhesion and penetration protein [Escherichia coli]	gi 1787452 gb AAC7 4286.1	30.7	21	110
						76%	3	275
HTHCB68	660309	5996	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	87%	3	443
						3	162	209
HTJAB35	880424	9601	HMMER 1.8	PFAM: Ank repeat	PF00023	35.64	242	325
HTJMT23	948518	6056	blastx.14	(AF182426) arylacetamide deacetylase [Rattus norvegicus]	gi 5923874 gb AAD5 6394.1 AF182426_1	58%	2	160
HTOAK34	966800	6081	HMMER	PFAM: Eukaryotic protein	PF00069	32.41	1020	1190

			1.8	kinase domain				
			blastx.14	(AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	gi 3452473 gb AAC7 1014.1	75%	954	1190
HTODG16	90952	6108	HMMER 2.1.1	PFAM: RasGEF domain	PF00617	148.5	4	402
			blastx.14	CDC25 [Saccharomyces kluuyveri]	gi 171187 gb AAA34 479.1	34%	13	399
HTOFT34	527144	6146	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.53	235	264
HTOHL35	537364	6173	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.52	4	33
HTOIY09	836003	6201	HMMER 1.8	PFAM: Insulin/IGF/Relaxin family	PF00049	7.08	61	123
HTSHF47	720403	6229	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	7.82	105	140
HTSHM38	972248	6230	HMMER 2.1.1	PFAM: EGF-like domain	PF00008	72	299	406
			blastx.14	(AB011532) MEGF6 [Rattus norvegicus]	gi 3449294 dbj BAA3 2462.1	88%	287	538
						50%	278	460
						53%	320	466
						42%	299	460
						42%	287	442
						43%	290	427
						40%	341	481
						46%	287	415
						70%	114	173
						66%	413	457



					50%	467	532
					61%	245	283
					35%	188	280
					47%	482	538
					52%	245	295
					39%	476	544
					61%	245	283
					31%	188	283
					50%	245	286
					29%	170	280
					55%	230	283
					69%	245	283
					53%	245	283
					50%	485	532
					35%	452	535
					47%	482	532
					47%	482	532
					50%	245	304
					31%	299	412
					70%	251	280
					58%	251	286
					30%	434	532
					58%	245	280
					53%	245	283
					37%	245	316
					63%	317	349
					75%	245	268
					47%	245	295
					37%	251	322
					54%	251	283
					31%	320	406

[illegible]

HTWCG65	869547	6260	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	60%	251	280
HTWEY30	918641	6299	blastx.14	(AF036548) RGC-32 [Rattus norvegicus]	gi 3800742 gb AAC6 8839.1	15.45	220	306
HTWJA59	812705	6314	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	88%	613	434
HTXCY84	924996	6359	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	4.95	172	219
HTXDW14	966588	6366	blastx.14	(AF038838) proline dehydrogenase [Klebsiella aerogenes]	gi 2766693 gb AAB9 5478.1	78%	47	241
HTXDX61	784768	6367	HMMER 2.1.1	(AB029335) HrPET-3 [Halocynthia roretzi]	gi 5360271 dbj BAA8 1908.1	45%	16	48
HTXFN69	869397	6394	HMMER 1.8	PFAM: Amidase	PF01425	41%	20	70
HTXGL73	529745	6403	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	54%	869	777
HTXJ168	912611	6420	blastx.14	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	45%	773	663
HTXJM73	783572	6425	HMMER 1.8	RAB14 [Rattus norvegicus]	gi 206535 gb AAA41 994.1	123.2	61	330
HTXKQ55	947789	6453	HMMER 2.1.1	PFAM: Bacterial mutT protein	PF00293	6.76	72	137
				PFAM: Peptidase family M3	PF01432	2.21	144	176
						97%	230	370
						60%	367	450
						59%	482	547
						52%	373	429
						2.87	97	123
						50.1	3	299

HTXNY74	918076	6525	blastx.14	mitochondrial intermediate peptidase precursor [Homo sapiens]	gi 1763642 gb AAC51231.1	96% 100%	3 335	302 367
HTXPT68	870074	6555	blastx.14	(AF078856) p47 [Homo sapiens]	gi 5531827 gb AAD44488.1	89% 96%	93 2	530 94
HTXQC36	961161	6560	HMMER 2.1.1	PFAM: NOL1/NOP2/sun family	PF011189	43.1	29	196
			blastx.14	(AB012223) ORF2 [Canis familiaris]	gi 2981631 dbj BAA25253.1	51% 57% 60% 42%	9 326 145 170	143 382 174 247
HTXRM86	975072	6575	HMMER 2.1.1	PFAM: Prokaryotic DNA topoisomerase	PF01131	99	243	446
			blastx.14	DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli]	gi 1742870 dbj BAA15551.1	51% 40%	177 3	440 158
HTXSB88	914627	6577	blastx.14	(AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	gi 4689132 gb AAD27775.1 AF077042_1	84%	559	771
HTXSR92	973095	6579	blastx.2	(AB016962) synGAP-b1 [Rattus norvegicus]	dbj BAA74972.1	60% 55%	302 1	421 60
HUJAM39	911399	6586	blastx.14	(AF051325) SH3 domain containing adaptor protein [Homo sapiens]	gi 4091782 gb AAC99298.1	46% 32%	170 709	310 885
HUJCM08	957784	6589	blastx.14	(AF015950) telomerase reverse transcriptase [Homo sapiens]	gi 2330017 gb AAC51672.1	100%	2	244
HUJAV06	966816	6597	blastx.14	(AF151854) CGI-96 protein [Homo sapiens]	gi 4929661 gb AAD34091.1 AF151854_1	88% 100% 68% 36%	595 464 537 561	521 396 481 487

HWAAF66	908541	6612	HMMER 2.1.1 blastx.14	PFAM: KRAB box	PF01352	65.3	90	278
				repressor protein [Homo sapiens]	gi 2789430 dbj BAA24380.1	54%	60	212
HWAAAY03	923734	6619	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.21	332	373
HWACA38	943074	6637	HMMER 1.8 blastx.14	PFAM: Bacterial mutT protein (AL033536) predicted using Genefinder; similar to 1 1 1 elegans]	PF00293	3.68	344	376
					gi 3947651 emb CAA22138.1	39% 52%	251 766	433 834
HWADF26	957347	6656	HMMER 1.8 blastx.2	PFAM: Lectin C-type domain short and long forms (AF175206) lectin-like receptor F1 [Homo sapiens]	PF00059	104.26	859	509
					gb AAF37804.1 AF175206_1	100%	3	596
HWAE20	868490	6691	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.01	251	313
HWAFW39	947915	6697	HMMER 2.1.1 blastx.2	PFAM: Peptidase family M1 (AF106037) adipocyte-derived leucine aminopeptidase [Homo sapiens]	PF01433	79.5	200	367
					gb AAF07395.1 AF106037_1	96%	200	367
HWAFX39	907631	6698	blastx.14	Zn-binding protein [Pleurodeles waltl]	gi 213868 gb AAA49614.1	46% 50%	118 19	354 120
HWAGM33	888685	6710	HMMER 2.1.1	PFAM: Plexin repeat	PF01437	25.8	898	1035

HWAGX37	959586	6711	blastx.14	unknown protein [Homo sapiens]	gi 1196433 gb AAA88038.1	47%	215	283
						34%	535	639
						42%	409	471
						29%	295	396
HWAHI10	960646	6714	blastx.14	retinoid X receptor interacting protein [Mus musculus]	gi 709961 gb AAC52167.1	62%	1215	583
						66%	513	343
						45%	642	412
						44%	1272	1198
						66%	1824	1798
HWAHS94	909667	6715	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD38043.1 AF151363_1	63%	278	484
						75%	487	510
HWBAL44	959449	6720	blastx.14	(AF151877) CGI-119 protein [Homo sapiens]	gi 4929707 gb AAD34114.1 AF151877_1	100%	531	424
HWBAQ16	868363	6722	HMMER 1.8	PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076	4.8	857	898
HWBBR65	747723	6741	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.15	185	205
HWBDM24	963498	6771	blastx.14	(AJ388555) hypothetical protein [Canis familiaris]	gi 5441611 emb CAB46854.1	83%	908	997
						100%	990	1040
						88%	837	863
HWBEX27	682583	6785	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	38.64	184	336
HYAAF33	915050	6820	blastx.14	(AF121858) sorting nexin 8 [Homo sapiens]	gi 4689256 gb AAD27831.1 AF121858_1	81%	273	434
						96%	217	306
						36%	172	270
HYAAS08	926017	6831	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47471.1	62%	203	156
						34%	84	7
						36%	125	69
						63%	150	118

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HWAF47	94858	6938	blastx.2	(AF010144) neuronal thread protein AD7c-NTP [Homo sapiens]	gb AAC08737.1	34% 44% 32% 34% 34% 63% 29% 38%	219 154 374 365 332 338 365 314	142 101 300 297 264 306 294 261
HWAU35	887166	6942	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047	23.2	40	273
			blastx	CMRF-35 antigen [Homo sapiens]	emb CAA46948.1	55% 59% 60% 38% 42%	7 169 400 346 316	162 279 474 399 372
HWAEG71	931547	6946	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	147.95	116	475
			blastx.2	rab-related GTP-binding protein [Rattus	gb AAA42000.1	98% 80%	86 477	493 569



HWAEC08	958115	6947	HMMER 2.1.1 blastx.14	norvegicus] PFAM: Spectrin repeat (AL080133) hypothetical protein [Homo sapiens]	PF00435 gi 5262574 emb CAB 45729.1	29.5	3	215
HWACY70	756888	6956	HMMER 2.1.1	PFAM: RIO1/ZK632.3/MJ0444 family	PF01163	96	280	552
HWABG11	949088	6971	HMMER 2.1.1 blastx.2	PFAM: Glucosamine-6- phosphate isomerase unnamed protein product [unidentified]	PF01182 emb CAA03416.1	225.7	67	381
HUUDR34	944903	6984	blastx.14	similar to SH3-binding protein [Homo sapiens]	gi 4826478 emb CAB 42896.1	82% 100% 77% 100%	2 571 552 596	550 594 578 616
HUUCJ02	940813	6986	blastx.14	(AF132984) nuclear pore complex interacting protein NPIP [Homo sapiens]	gi 4959568 gb AAD3 4394.1 AF132984_1	99% 89% 71% 58% 87% 100% 54% 60% 81% 83% 40% 100% 90%	770 417 300 226 278 261 261 258 181 152 229 152 192	417 250 187 119 231 226 196 199 149 117 149 126 163

HTXOO15	869261	7011	HMMER 2.1.1	PFAM: Ubiquitin family	PF00240	66%	300	274
HTXLS08	958357	7023	blastx.14	(AF090989) high-risk human papilloma viruses E6 1 alpha [Homo sapiens]	gi 4151328 gb AAD1 2543.1	48% 68% 41% 57% 70% 27%	745 1006 1 511 427 580	987 1146 237 645 477 645
HTWKB07	952841	7085	blastx.14	(AF003535) ORF2-like protein [Homo sapiens]	gi 2197085 gb AAD0 4635.1	60% 75% 50% 33% 70%	25 259 205 36 167	84 294 258 116 196
HTWJH08	790185	7087	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	61%	197	51
HTWJH08	846554	9615	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	61%	197	51
HTWJF50	911448	7089	blastx.14	myosin I [Rattus norvegicus]	gi 3724141 emb CAA 50871.1	48% 53% 55% 46% 39% 50%	1009 334 732 863 40 686	1428 681 851 1012 108 715
HTWFAQ19	586124	7091	HMMER 2.1.1	PFAM: Sema domain	PF01403	62.9	14	184
HTOIA82	844319	7198	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.25	50	82
HTOHI14	659280	7204	HMMER	PFAM: Asparaginase	PF01112	20.7	140	217

HTODM08	960113	7222	2.1.1 blastx.14	(AF106069) deubiquitinating enzyme [Homo sapiens]	gi 5814097 gb AAD5 2099.1 AF106069_1	33%	5	367
HTHBY73	946168	7282	blastx.2	(AK001868) unnamed protein product [Homo sapiens]	dbj BAA91951.1	52% 45%	4 162	183 332
HTGEX10	963862	7305	HMMER 2.1.1 blastx.14	PFAM: SET domain	PF00856	105.2	580	960
HTGEA37	908606	7311	blastx.14	(AC005065) determined by GENSCAN prediction and 1	gi 4153862 gb AAD0 4721.1	65% 40%	601 337	1017 477
HTAIF22	910040	7364	HMMER 2.1.1 blastx.14	(AF001293) aiolos [Mus musculus] PFAM: RhoGEF domain	gi 2150044 gb AAB5 8795.1  PF00621	80%	1	216
HTAIF11	965738	7365	blastx.14	(AL022271) similar to Guanine nucleotide exchange 1 1 1 this g (AF061555) ubiquitin- protein ligase E3-alpha [Mus musculus]	gi 3876654 emb CAA 18349.1  gi 3170887 gb AAC4 0165.1	64% 48% 50%	281 6 297	397 293 392
HTAEV23	959129	7369	HMMER 2.1.1 blastx.14	PFAM: WW domain This gene is novel. [Homo sapiens]	PF00397 gi 603953 dbj BAA07 893.1	25.9 89%	478 823	386 359
HTAEP05	932459	7370	blastx.14	Pro-Pol-dUTPase polyprotein [Mus musculus]	gi 2065210 emb CAA 73251.1	76% 48% 47% 44%	225 406 3 500	275 510 59 553

HTABK47	720684	7379	HMMER 2.1.1	PFAM: Monooxygenase	PF01360	77%	386	412
HSYCV01	940661	7408	HMMER 1.8	PFAM: Hydroxymethylglutaryl- coenzyme A reductase	PF00369	7.29	448	492
HSAWR08	959943	7458	blastx.14	(AL110271) hypothetical protein [Homo sapiens]	gi 5817084 emb CAB 53709.1	98%	123	287
HSAUL84	908440	7504	HMMER 2.1.1	PFAM: gag gene protein p24 (core nucleocapsid protein)	PF00607	43.3	105	302
HNHOF94	948720	7551	blastx.14	gag protein [Human endogenous retrovirus K]	gi 1780975 emb CAA 71418.1	83%	135	299
			blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	60%	24	152
HNHNP81	928378	7554	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	58.09	233	511
			blastx.2	(AF091575) olfactory receptor [Rattus norvegicus]	gb AAC64595.1	61%	236	505
HNHLC01	915363	7581	blastx.14	unknown protein [Homo sapiens]	gi 1196431 gb AAA8 8036.1	52%	502	618
			blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	46%	5	82
HNHGV62	743400	7603	blastx.2			40%	57	131
						36%	133	207
						61%	219	257
						46%	260	304
						62%	52	285
						76%	287	349

HNHGE31	698046	7624	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.3	83	109
HNHFV49	975415	7644	blastx.2	hypothetical protein (L1H 3' region) - human	pir B34087 B34087	81% 71% 90%	483 227 217	190 6 188
HNHFH24	903741	7657	HMMER 2.1.1	PFAM: Sodium:neurotransmitter symporter family	PF00209	37.2	208	306
			blastx.14	(AF075266) orphan transporter isoform B9 [Mus musculus]	gi 3347930 gb AAC2 7761.1	76% 27%	187 414	327 467
HNHDF07	953883	7702	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041	7.48	242	319
HNHDC29	904546	7704	blastx.14	contactin associated protein [Homo sapiens]	gi 1857708 gb AAB4 8481.1	98%	219	7
HNHIC32	861673	7716	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	133.17	195	545
			blastx.2	(AF112461) G protein- coupled receptor 57 [Homo sapiens]	gb AAF27279.1 AF1 12461_1	100% 100% 100%	189 112 56	551 186 112
HNHIC32	956105	9645	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	133.17	951	601
			blastx.2	(AF112461) G protein- coupled receptor 57 [Homo sapiens]	gb AAF27279.1 AF1 12461_1	100% 100% 100%	555 478 422	917 552 478
HNHBF47	949027	7731	HMMER 1.8	PFAM: Cadherin	PF00028	44.76	668	522
			blastx.2	(AB028499) Flamingo 1	dbj BAA84070.1	96%	409	666

1496

HNHAF61	742116	7745	HMMER 1.8 blastx.2	PFAM: Cadherin  (AF152473) protocadherin alpha C1 short form protein [Homo sapiens]	PF00028  gb AAD43734.1 AF1 52473_1	39% 46.67	412 330	480 461
HNHAF61	955094	9649	blastx.14	(AF152303) protocadherin alpha C1 [Homo sapiens]	gi 5456892 gb AAD4 3697.1	75% 84% 33% 93% 40%	81 173 87 1 10	677 364 686 84 75
HNHAF61	955094	9649	blastx.14	(AF152303) protocadherin alpha C1 [Homo sapiens]	gi 5456892 gb AAD4 3697.1	98% 40% 42% 32% 37% 100% 77% 30% 89% 35% 40% 36% 50%	325 715 499 778 724 225 176 496 269 895 568 717 499	1071 987 660 1023 867 275 229 684 325 1011 663 791 540
HNGOZ40	969158	7757	blastx.14	(AF155098) NY-REN-8 antigen [Homo sapiens]	gi 5360091 gb AAD4 2864.1 AF155098_1	78%	599	477
HNGNY02	918626	7769	HMMER 1.8	PFAM: FAD/NAD- binding domain in oxidoreductases	PF00175	4.43	366	440
HNGND01	915294	7778	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.07	464	490
HNGMW65	950173	7781	blastx.2	(AF010144) neuronal thread protein AD7c-NTP	gb AAC08737.1	62% 67%	340 340	143 248

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HNGFF50	941480	7879	blastx.14	(AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus]	gi 4186073 emb CAA.09423.1	45%	193	2
HNGEO79	951489	7897	HMMER 1.8	PFAM: IG (immunoglobulin) superfamily	PF00047	33.71	290	466
			blastx	(AF143185) high affinity immunoglobulin gamma Fc 1	gb AAD34946.1 AF143185_1	54% 41% 77% 36%	287 404 230 140	385 520 283 214
HNGEI11	967314	7902	blastx.14	pol polyprotein [Baboon endogenous virus]	gi 509838 gb AAA87332.1	70% 42% 53%	258 39 324	317 152 368
HNGDM11	967512	7933	blastx.14	reverse transcriptase [Homo sapiens]	gi 439877 gb AAB02291.1	36% 50% 47% 20%	381 276 154 210	292 205 104 82
HNGDA08	959964	7952	HMMER 1.8	PFAM: Zinc finger, CCHC class	PF00098	5.01	261	284
HNGAZ08	959977	7973	blastx.14	p40 [Homo sapiens]	gi 2072966 gb AAC51272.1	45% 40%	391 93	320 19

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